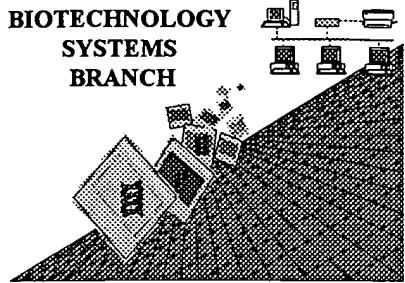


C. Kaufman

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/157,289A

Art Unit / Team No.: 1646

Date Processed by STIC: 6/14/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
-----------------------	-----------------------------

SERIAL NUMBER: 09/157,289A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | |
|----|--|
| 1 | Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. |
| 8 | Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and <u>which residue n or Xaa represents.</u> |
| 11 | Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response. |
| 12 | Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999
TIME: 15:31:19

Input Set: I157289A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: ASHKENAZI, AVI J.
2 BOTSTEIN, DAVID
3 DODGE, KELLY H.
4 GURNEY, AUSTIN L.
5 KIM, KYUNG JIN
6 LAWRENCE, DAVID A.
7 PITTI, ROBERT
8 ROY, MARGARET A.
9 TUMAS, DANIEL B.
10 WOOD, WILLIAM I.
11 GENENTECH INC.
12 <120> TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
13 <130> FILE REFERENCE: 11669.31US03
14 <140> CURRENT APPLICATION NUMBER: US/09/157,289A
15 <141> CURRENT FILING DATE: 1998-09-18
16 <150> EARLIER APPLICATION NUMBER: 60/059,288
17 <151> EARLIER FILING DATE: 1997-09-18
18 <150> EARLIER APPLICATION NUMBER: 60/094,640
19 <151> EARLIER FILING DATE: 1998-07-30
20 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
23 <211> LENGTH: 300
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
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28 1 5 10 15
29 Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
30 20 25 30
31 Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
32 35 40 45
33 Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
34 50 55 60
35 Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
36 65 70 75 80
37 Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr Cys Asn Val Leu Cys Gly
38 85 90 95
39 Glu Arg Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
40 100 105 110
41 Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
42 115 120 125
43 His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
44 130 135 140

APR 24

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999
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Input Set: I157289A.RAW

45 Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
 46 145 150 155 160
 47 Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
 48 165 170 175
 49 Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
 50 180 185 190
 51 Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
 52 195 200 205
 53 Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
 54 210 215 220
 55 Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
 56 225 230 235 240
 57 Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
 58 245 250 255
 59 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
 60 260 265 270
 61 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
 62 275 280 285
 63 Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
 64 290 295 300

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<211> LENGTH: 1114

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: @ nt 1090

<400> SEQUENCE: 2

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 aggccctgtcg ctgctgtgcc tgggtttggc gctgcctgcc ctgctgccgg tgccggctgt 180
 acgcggagtgc gcagaaaacac ccacacctacc cttggcgggac gcagagacag gggagcggct 240
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 cacccacaac cgtgcctgcc gctgccgcac cggcttcttc ggcacgcgtg gtttctgctt 480
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 cacgcagtgc cagccgtgcc ccccaggcac cttctcagcc agcagctcca gtcagagca 600
 gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc caggctcttc 660
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 agctgaggag tggagcgtg ccgtcatcga ctttgtggct ttccaggaca tctccatcaa 780
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 ggcggggccgc gcccgttgc agctgaagct ggtcgccgg ctcacggagc tcctggggc 900
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 gctggagcgg agcgtccgtg agcgttcct ccctgtgcac tgatcctggc ccccttttat 1020
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 90 atgaggttt taaaaaaaaaaaaaaa aaaaaaaa aaaa 1114

91 <210> SEQ ID NO 3

92 <211> LENGTH: 491

93 <212> TYPE: DNA

94 <213> ORGANISM: Unknown

Please see item 10 on
Error summary sheet
what does this mean?

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999
TIME: 15:31:19

Input Set: I157289A.RAW

95 <220> FEATURE:
 96 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 97 <220> FEATURE:
 98 <223> OTHER INFORMATION: (61) 73, 86, 98 what does "n" represent at
 99 <400> SEQUENCE: 3 162 these locations?
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 102 gggcttgcga cgccacccac aaccgtgcct ggcgtccgc caccggcttc ttgcgcacag 180
 103 ctggtttctg cttggagcac gcacgtgtc cacctgggtgc cggcgtgatt gccccgggca 240
 104 ccccgagcca gaacacgcac tgccctagccg tgcccccag gcaccttctc agccagcagc 300
 105 tccagcttag agcagtgcac gccccaccgc aactgcacgg ccctgggcct gccccta 360
 106 gtgccaggct ctccctccca tgacaccctg tgcaccagct gcactggctt cccctcagc 420
 107 accagggtac caggagctga ggagtgtgag cgtgccgtca tcgactttgt ggcttccag 480
 108 gacatctcca t 491
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 111 <212> TYPE: DNA
 112 <213> ORGANISM: Unknown
 113 <220> FEATURE:
 114 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 115 <400> SEQUENCE: 4
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 117 ctacctggag cgc 73
 118 <210> SEQ ID NO 5
 119 <211> LENGTH: 271
 120 <212> TYPE: DNA
 121 <213> ORGANISM: Unknown
 122 <220> FEATURE:
 123 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 124 <220> FEATURE: 42 122
 125 <223> OTHER INFORMATION: (52) 62, 73, 86, 98, 106, 120, (121), 153, 167, 184,
 126 220 and 233
 127 <400> SEQUENCE: 5 what does "n" represent?
 128 gcccagacag ccccacgacg tggccgt gtccaccgcg ccactacacg cagttctgga 60
 W--> 129 antaactgga gcncgtccgc tactgnaacg tcctctgnng ggagcgtgag gaggaggca 120
 W--> 130 gggcttgcga cgccacccac aaccgtgcct gcngcgtcag caccggnttc ttgcgcacag 180
 W--> 131 ctggtttctg cttggagcac gcacgtgtc cacctgggtgn cggcgtgatt gcncgggca 240
 132 ccccgagcca gaacacgcac gcaaaggcgt g 271
 133 <210> SEQ ID NO 6
 134 <211> LENGTH: 201
 135 <212> TYPE: DNA
 136 <213> ORGANISM: Unknown
 137 <220> FEATURE:
 138 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 139 <220> FEATURE:
 140 <223> OTHER INFORMATION: 182 what does "n" represent?
 141 <400> SEQUENCE: 6
 142 gcagttctgg aactacctgg agcgctgcgc ctactgcaac gtccctctgcg gggagcgtga 60
 143 ggaggaggca cgggcttgcc acgccaccca caaccgtgcc tgccgtgcc gcacccggctt 120
 144 ctgcgcac gctggttct gctggagca cgcacatgtt ccacctgggt cggcgtgat 180

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RAW SEQUENCE LISTING
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Input Set: I157289A.RAW

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 150 <220> FEATURE:
 151 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 152 <220> FEATURE:
 153 <223> OTHER INFORMATION: (141) 142 what does "n" represent?
 154 <400> SEQUENCE: 7
 155 gaggggccccc caggagtggt ggccggaggt gtggcagggg tcaggttgct ggtcccagcc 60
 156 ttgcaccttg agctaggaca ccagttcccc tgaccctgtt ctcccttcct ggctgcagggc 120
 W--> 157 accccccagcc agaacacgcga gnccagccgt gccccccagg cacttctca gccagcagct 180
 158 ccagctcaga gcagtgccag ccccacggca actgcacggc cctggcctg gccctcaatg 240
 159 tgccaggctc ttccctccat gacaccctgt gcaccag 277
 160 <210> SEQ ID NO 8
 161 <211> LENGTH: 199
 162 <212> TYPE: DNA
 163 <213> ORGANISM: Unknown
 164 <220> FEATURE:
 165 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 166 <400> SEQUENCE: 8
 167 gcatcgtgtc cacctgggtgc cggcgtgatt gccccgggca ccccccggcca gaacacgcag 60
 168 gccttagccgt gccccccagg cacttctca gccagcagct ccagctcaga gcagtgcag 120
 169 ccccacggca actgcacggc cctggcctg gccctcaatg tgccaggctc ttccctccat 180
 170 gacaccctgt gcaccagct 199
 171 <210> SEQ ID NO 9
 172 <211> LENGTH: 226
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Unknown
 175 <220> FEATURE:
 176 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
 177 <220> FEATURE: 4, 9, 12,
 178 <223> OTHER INFORMATION: 64, 69, 72, 175 (165) what does "n" represent?
 179 <400> SEQUENCE: 9
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 181 accgcaactg cacggccctg ggcctggccc tcaatgtgcc aggctttcc tcccatgaca 120
 W--> 182 cgcgtgtgcac cagctgact ggcttcccc tcaagcaccag ggtancagga gctgaggagt 180
 183 gtgagcgtgc cgtcatcgac tttgtggctt tccaggacat ctccat 226
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 185 <211> LENGTH: 283
 186 <212> TYPE: DNA
 187 <213> ORGANISM: Homo sapiens
 188 <220> FEATURE: 27
 189 <223> OTHER INFORMATION: (37) 64, 140 what does "n" represent?
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 W--> 192 gcnntcccc cagggcacctt ctcagccagc agctccagct cagagcagtg ccagccccc 120
 W--> 193 cgcaactgca acggccctgg ctggccctca atgtgccagg ctcttctcc catgacaccc 180
 194 tgtgcaccag ctgcactggc ttcccccata gacccagggt accaggagct gaggagtgtg 240

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999
TIME: 15:31:19

Input Set: I157289A.RAW

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196 <210> SEQ ID NO 11
197 <211> LENGTH: 21
198 <212> TYPE: DNA
199 <213> ORGANISM: Unknown
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
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204 <210> SEQ ID NO 12
205 <211> LENGTH: 22
206 <212> TYPE: DNA
207 <213> ORGANISM: Unknown
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
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212 <210> SEQ ID NO 13
213 <211> LENGTH: 53
214 <212> TYPE: DNA
215 <213> ORGANISM: Unknown
216 <220> FEATURE:
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221 <211> LENGTH: 24
222 <212> TYPE: DNA
223 <213> ORGANISM: Unknown
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
226 <400> SEQUENCE: 14
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228 <210> SEQ ID NO 15
229 <211> LENGTH: 17
230 <212> TYPE: DNA
231 <213> ORGANISM: Unknown
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
234 <400> SEQUENCE: 15
235 cttcttcgcg cacgctg 17
236 <210> SEQ ID NO 16
237 <211> LENGTH: 16
238 <212> TYPE: DNA
239 <213> ORGANISM: Unknown
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
242 <400> SEQUENCE: 16
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Input Set: I157289A.RAW

Line ? Error/Warning

Original Text

90 W "N" or "Xaa" used: Feature required
101 W "N" or "Xaa" used: Feature required
128 W "N" or "Xaa" used: Feature required
129 W "N" or "Xaa" used: Feature required
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131 W "N" or "Xaa" used: Feature required
145 W "N" or "Xaa" used: Feature required
157 W "N" or "Xaa" used: Feature required
180 W "N" or "Xaa" used: Feature required
182 W "N" or "Xaa" used: Feature required
191 W "N" or "Xaa" used: Feature required
192 W "N" or "Xaa" used: Feature required
193 W "N" or "Xaa" used: Feature required

atgaggtnn taaaaaaaaaaaaaaa aaaaaaaaaaaa aaaa
antaactgga gcnctgccgc tactgnaacg tcctctgn
gccgagacag ccccacgacg tgtggcccggt gtccaccg
antaactgga gcnctgccgc tactgnaacg tcctctgn
gngcttgcca cgccacccac aaccgcgcct gcnngctgc
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tnccccgggc accccccagcc a
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cgctgtgcac cagctgcact ggcttcccccc tcagcacc
cttgtccacc tggtgccggc gtgattnccc gggcaccc
gcnntcccccc caggcacctt ctcagccagc agctccag
cgcaactgca acgcccctggn ctggccctca atgtgcca